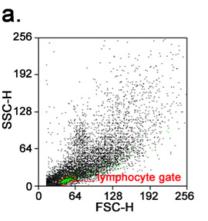
Table 1. Primer sequences used for real time PCR (3' to 5')

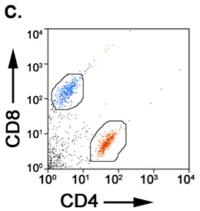
Gene target	Forward	Reverse
Cyclophilin A	GTGGTCTTTGGGAAGGTGAA	TTACAGGACATTGCGAGCAG
Cd11c	CTGGATAGCCTTTCTTCTGCTG	GCACACTGTGTCCGAACTC
IL-12p40	GGAGACACCAGCAAAACGAT	GATTCAGACTCCAGGGGACA
IFN-γ	TCTGGAGGAACTGGCAAAAG	TTCAAGACTTCAAAGAGTCTGAGG
IL-4	TCAACCCCCAGCTAGTTGTC	TGTTCTTCGTTGCTGTGAGG
IL-18	CAGTGAACCCCAGACCAGAC	GGCAAGCAAGAAAGTGTCCT
IL-13	CCAGGTCCACACTCCATACC	TGCCAAGATCTGTGTCTCTCC
RANTES	CAGGAGCAAGTGCTCCAATCTT	TTCTTGAACCCACTTCTTCTCTGG
CD3	AGGCACTGTAGCCCAGACAAATA	AGCCACTTGATAGTCTTGTCAGTCA
IP-10/CXCL10	GCTGCCGTCATTTTCTGC	TCTCACTGGCCCGTCATC
MIG/CXCL9	CTTTTCCTTTTGGGCATCAT	CGATCGTGCATTCCTTATCA
I-A	GTGGTGCTGATGGTGCTG	CCATGAACTGGTACACGAAATG

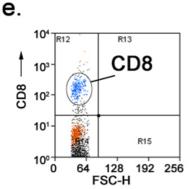
Supplement Figure Legends.

Figure S-1. Gating procedures used for FACS analyses. (**a**) Ungated and uncompensated plots showing forward and side scatter properties and (**b**) positive CD3-staining; used to define the lymphocyte (R1) gate for each SVC sample. For each experiment, matched isotype-conjugated controls were used to define non-specific background fluorescence events, which were excluded (not shown). (**c**) Colored gating [red for anti-CD4-PE(FL2), and blue for anti-CD8-PECy5(FL3)] indicates the positive events counted within the SVC population of the lymphocyte gate for cell surface markers of interest. Dot plots showing how single fluorescence channels were used to quantify positive events.

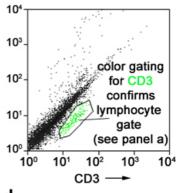
Figure S-2. Temporal dynamics of mRNA levels of Th1-associated genes and IL-13 in whole eAT through 20 weeks of high fat diet (HFD). (**a**) IP-10, (**b**) Mig, (**c**) IL-18, and (**d**) IL-13. Data are expressed as fold change (mean ± sem) relative to low fat diet (LFD). n = 3 to 4, LFD and n = 4, HFD mice at each time point. Bars identified by different letters are significantly different ($P \le 0.05$). [#], $P \le 0.05$ for comparison between diets at the indicated time point.







b.



d.

